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TRANSMITTAL
FORM

(to be used for all correspondence after initial filing)

Total Number of Pages in This Submission

Application Number 09/597,796

Filing Date June 20, 2000

First Named Inventor Skeiky, Yasir

Group Art Unit 1645

Examiner Name Swartz, Rodney P.

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TECH CENTER 1600/2900

Attorney Docket Number 014058-009050US

ENCLOSURES (check all that apply)

 Fee Transmittal Form Fee Attached Amendment / Reply After Final Affidavits/declaration(s) Extension of Time Request Express Abandonment Request Information Disclosure Statement Certified Copy of Priority Document(s) Response to Missing Parts/ Incomplete Application Response to Missing Parts under 37 CFR 1.52 or 1.53 Assignment Papers
(for an Application) Drawing(s) Licensing-related Papers Petition Petition to Convert to a Provisional Application Power of Attorney, Revocation Change of Correspondence Address Terminal Disclaimer Request for Refund CD, Number of CD(s) After Allowance Communication to Group Appeal Communication to Board of Appeals and Interferences Appeal Communication to Group (Appeal Notice, Brief, Reply Brief) Proprietary Information Status Letter Other Enclosure(s)
(please identify below):

Return Postcard; Communication Under 37 CFR 1.821-1.825 and Amendment; disk containing sequence listing; copy of Notice to Comply..

Remarks

The Commissioner is authorized to charge any additional fees to Deposit Account 20-1430.

SIGNATURE OF APPLICANT, ATTORNEY, OR AGENT

Firm and Individual name

Townsend and Townsend and Crew LLP

Annette S. Parent

Reg. No. 42,058

Signature

Date

December 4, 2002

CERTIFICATE OF MAILING

I hereby certify that this correspondence is being deposited with the United States Postal Service with sufficient postage as first class mail in an envelope addressed to: Commissioner for Patents, Washington, D.C. 20231 on this date:

12/04/02

Typed or printed name

Dana Kane

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ASP/14

APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
09/597,796	06/20/2000	Yasir Skeiky	014058-009050US	6269

20350 7590 11/04/2002

TOWNSEND AND TOWNSEND AND CREW, LLP
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EIGHTH FLOOR
SAN FRANCISCO, CA 94111-3834

EXAMINER

SWARTZ, RODNEY P

ART UNIT

PAPER NUMBER

1645

DATE MAILED: 11/04/2002

15

Response Due ~~SCC LIST 12/14/02 ALB~~

Please find below and/or attached an Office communication concerning this application or proceeding.



UNITED STATES DEPARTMENT OF COMMERCE
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Washington, D.C. 20231

SERIAL NUMBER	FILING DATE	FIRST NAMED APPLICANT	ATTORNEY DOCKET NO.
09/597,796			

EXAMINER	
Rodney P. Swartz, Ph.D.	
ART UNIT	PAPER NUMBER
1645	

DATE MAILED:

Please find below a communication from the EXAMINER in charge of this application

Commissioner of Patents

This Application contains sequence disclosures that are encompassed by the definitions for nucleotide and/or amino acid sequences set forth in 37 C.F.R. § 1.821(a)(1) and (a)(2). However, this application fails to comply with the requirements of 37 CFR §§ 1.821 - 1.825 for the reason(s) set forth on the attached Notice To Comply With Requirements For Patent Applications Containing Nucleotide Sequences And/Or Amino Acid Sequence Disclosures.

Any inquiry concerning this communication should be directed to Examiner Rodney P. Swartz, Ph.D., Art Unit 1645, whose telephone number is (703) 308-4244. If unable to reach the examiner, Lynette Smith, SPE, can be contacted at (703) 308-3909.

Any questions regarding compliance with the sequence rules requirements specifically should be directed to the departments listed at the bottom of the Notice To Comply.

Any inquiry of a general nature or relating to the status of this application should be directed to the Group receptionist whose telephone number is (703) 308-0196.

APPLICANT IS GIVEN ONE MONTH FROM THE DATE OF THIS LETTER WITHIN WHICH TO COMPLY WITH THE SEQUENCE RULES, 37 C.F.R. §§ 1.821 - 1.825. Failure to comply with these requirements will result in ABANDONMENT of the application under 37 C.F.R. § 1.821(g). Extensions of time may be obtained by filing a petition accompanied by the extension fee under the provisions of 37 C.F.R. § 1.136. In no case may an applicant extend the period for response beyond the six month statutory period. Direct the response to the undersigned. Applicant is requested to return a copy of the attached Notice to Comply with the response.

Rodney P. Swartz, Ph.D.
November 4, 2002



Application No. 09/597,796

**NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING
NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES**

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 CAR §1.821 - §1.825 for the following reason(s):

[X] 1. This application clearly fails to comply with the requirements of 37 CAR §1.821 - §1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990, and at 55 FR 18230, May 1, 1990.

[] 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 CAR §1.821(c).

[] 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 CAR §1.821(e).

[X] 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 CAR §1.822 and/or §1.823, as indicated on the attached copy of the marked-up "Raw Sequence Listing".

[] 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A substitute computer readable form must be submitted as required by 37 CAR §1.825(d).

[] 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 CAR §1.821(e).

[] 7. Other: _____

APPLICANT MUST PROVIDE:

[X] An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".

[X] An initial or substitute paper copy of the "Sequence Listing", as were as an amendment directing its entry into the specification.

[X] A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 CAR §1.821(e) or §1.821(f) or §1.821(g) or §1.825(b) or §1.825(d).

FOR QUESTIONS REGARDING COMPLIANCE WITH THESE REQUIREMENTS, PLEASE CONTACT:

For Rules Interpretation, call (703) 308-1123
For CRF Submission help, call (703)308-4212
For Patentin Software help, call (703) 557-0400

PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR RESPONSE.

Raw Sequence Listing Error Summary

<u>ERROR DETECTED</u>	<u>SUGGESTED CORRECTION</u>	<u>SERIAL NUMBER: 09/597,796B</u>
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO'S		
1 <input type="checkbox"/> Wrapped Nucleic <input type="checkbox"/> Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 <input type="checkbox"/> Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 <input type="checkbox"/> Misaligned Amino <input type="checkbox"/> Numbering	The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.	
4 <input type="checkbox"/> Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 <input type="checkbox"/> Variable Length	Sequence(s) <input type="checkbox"/> contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 <input type="checkbox"/> PatentIn 2.0 <input type="checkbox"/> "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) <input type="checkbox"/> . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 <input type="checkbox"/> Skipped Sequences <input type="checkbox"/> (OLD RULES)	Sequence(s) <input type="checkbox"/> missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading). (xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped	
	Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 <input type="checkbox"/> Skipped Sequences <input type="checkbox"/> (NEW RULES)	Sequence(s) <input type="checkbox"/> missing. If Intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
9 <input type="checkbox"/> Use of n's or Xaa's <input type="checkbox"/> (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.	
10 <input type="checkbox"/> Invalid <213> <input type="checkbox"/> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence	
11 <input type="checkbox"/> Use of <220>	Sequence(s) <input type="checkbox"/> missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 <input type="checkbox"/> PatentIn 2.0 <input type="checkbox"/> "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 <input type="checkbox"/> Misuse of n	n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.	

1600

RAW SEQUENCE LISTING DATE: 01/15/2002
 PATENT APPLICATION: US/09/597,796B TIME: 12:32:10

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 Output Set: N:\CRF3\01152002\I597796B.raw

3 <110> APPLICANT: Skeiky, Yasir
 4 Reed, Steven
 5 Alderson, Mark
 6 Corixa Corporation
 Does Not Comply
 Corrected Diskette Needed
 8 <120> TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
 10 <130> FILE REFERENCE: 014058-009050US
 12 <140> CURRENT APPLICATION NUMBER: US 09/597,796B
 13 <141> CURRENT FILING DATE: 2001-06-20
 14 <150> PRIOR APPLICATION NUMBER: US 09/056,556
 15 <151> PRIOR FILING DATE: 1998-04-07
 16 <150> PRIOR APPLICATION NUMBER: US 09/223,040
 17 <151> PRIOR FILING DATE: 1998-12-30
 18 <150> PRIOR APPLICATION NUMBER: WO PCT/US99/07717
 19 <151> PRIOR FILING DATE: 1999-04-07
 20 <150> PRIOR APPLICATION NUMBER: US 09/287,849
 21 <151> PRIOR FILING DATE: 1999-04-07
 22 <150> PRIOR APPLICATION NUMBER: US 60/158,338
 23 <151> PRIOR FILING DATE: 1999-10-07
 24 <150> PRIOR APPLICATION NUMBER: US 60/158,425
 25 <151> PRIOR FILING DATE: 1999-10-07
 26 <150> PRIOR APPLICATION NUMBER: US 60/158,338
 27 <151> PRIOR FILING DATE: 1999-10-07
 28 <150> PRIOR APPLICATION NUMBER: US 60/158,425
 29 <151> PRIOR FILING DATE: 1999-10-07
 30 <160> NUMBER OF SEQ ID NOS: 30
 31 <170> SOFTWARE: PatentIn Ver. 2.1
 32 <210> SEQ ID NO: 1
 33 <211> LENGTH: 588
 34 <212> TYPE: DNA
 35 <213> ORGANISM: Mycobacterium tuberculosis
 36 <220> FEATURE:
 37 <223> OTHER INFORMATION: Ra35, N-terminus of MTB32A (TbRa35FL)
 38 <220> FEATURE:
 39 <221> NAME/KEY: CDS
 40 <222> LOCATION: (1)..(588)
 41 <223> OTHER INFORMATION: Ra35
 42 <400> SEQUENCE: 1
 43 gccccgcccgg ccttgcgcga ggaccgggttc gccgacttcc cccgcgtgcc cctcgaccgg 60
 44 tccgcgtatgg tcgccccaaatggggccacacag gtggtaacaaca tcaacacccaa actgggctac 120
 45 aacaacgccc tgggcgcggg gaccggcattc gtcatcgatc ccaacgggtt cgtgctgacc 180
 46 aacaaccacg tgatcgccggg cgccaccggac atcaatgcgt tcagcgtcgg ctccggccaa 240
 47 acctacggcg tcgatgtggt cgggtatgac cgcacccagg atgtcgcgtt gctgcagctg 300
 48 cgcgggtccgg gtggcctacc atcggcggcg atcgggtggcg gcgtcgcgtt tggtagcccc 360
 49 gtcgtcgcga tggcaacacag cgggtggcag ggcggaaacgc cccgtgcgtt gcctggcagg 420
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 51 ttgaacgggt tgatccagtt cgatgccgcg atccagcccg gtgattcggg cggggccgc 540
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 53 <210> SEQ ID NO: 2
 54 <211> LENGTH: 195
 55 <212> TYPE: PRT
 56 <213> ORGANISM: Mycobacterium tuberculosis

PP 3, b-8

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/597,796B

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TIME: 12:32:10

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67 <223> OTHER INFORMATION: Ra35, N-terminus of MTB32A (TbRa35FL)

70 <400> SEQUENCE: 2

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72 1 5 10 15
73 Pro Leu Asp Pro Ser Ala Met Val Ala Gln Val Gly Pro Gln Val Val
74 20 25 30
75 Asn Ile Asn Thr Lys Leu Gly Tyr Asn Asn Ala Val Gly Ala Gly Thr
76 35 40 45
77 Gly Ile Val Ile Asp Pro Asn Gly Val Val Leu Thr Asn Asn His Val
78 50 55 60
79 Ile Ala Gly Ala Thr Asp Ile Asn Ala Phe Ser Val Gly Ser Gly Gln
80 65 70 75 80
81 Thr Tyr Gly Val Asp Val Val Gly Tyr Asp Arg Thr Gln Asp Val Ala
82 85 90 95
83 Val Leu Gln Leu Arg Gly Ala Gly Gly Leu Pro Ser Ala Ala Ile Gly
84 100 105 110
85 Gly Gly Val Ala Val Gly Glu Pro Val Val Ala Met Gly Asn Ser Gly
86 115 120 125
87 Gly Gln Gly Gly Thr Pro Arg Ala Val Pro Gly Arg Val Val Ala Leu
88 130 135 140
89 Gly Gln Thr Val Gln Ala Ser Asp Ser Leu Thr Gly Ala Glu Glu Thr
90 145 150 155 160
91 Leu Asn Gly Leu Ile Gln Phe Asp Ala Ala Ile Gln Pro Gly Asp Ser
92 165 170 175
93 Gly Gly Pro Val Val Asn Gly Leu Gly Gln Val Val Gly Met Asn Thr
94 180 185 190

95 Ala Ala Ser

96 195

99 <210> SEQ ID NO: 3

100 <211> LENGTH: 1872

101 <212> TYPE: DNA

102 <213> ORGANISM: *Mycobacterium tuberculosis*

104 <220> FEATURE:

105 <223> OTHER INFORMATION: MTB32A (TbRa35FL) cDNA

107 <400> SEQUENCE: 3

108 gactacgttg gtgtagaaaa atcctgccgc ccggaccctt aaggctggga caatttctga 60
109 tagtacccca gacacaggag gttacggat gagcaattcg cgccgcgcct cactcaggtg 120
110 gtcatggttc ctgagcgtgc tggctgcgt cggtctggc ctggccacgg cgccggccca 180
111 ggcggccccc ccggccttgt cgccaggaccg gttcggcgc acatccgc tgccccctcga 240
112 cccgtccgcg atggtcgccc aagtggcgc acagggtggtc aacatcaaca ccaaactggg 300
113 ctacaacaac gccgtggcg ccgggaccgg catcgatcg gatccaaacg gtgtcgtgct 360
114 gaccaacaac cacgtatcg cggcgccac cgacatcaat gcgttcagcg tcggctccgg 420
115 ccaaaccctac ggcgtcgatg tggtcgggta tgaccgcacc caggatgtcg cgggtctgca 480
116 gctgcgcgtt gccgtggcc tggcgatcg ggcgtcgatg ggcggcgatcg cgggtggta 540
117 gcccgtcgatcg gcgatgggca acagggtggc gcaggccggc acgccccgtg cgggtgcctgg 600
118 cagggtggtc ggcgtcgatcg aaaccgtgca ggcgtcgatg tggcgatcg gtcggaaaga 660
119 gacattgaac gggttgatcc agttcgatgc cgcaatcccg cccggatcgatt cggggggggcc 720
120 cgtcgatcg ggcgtcgatcg aggtggtcgg tatgaacacg gccgtcgatcg gtcggaaaga 780
121 gctgtcccaac ggtggcagg gattcgccat tccgtcgatcg caggcgatcg cgtcgatcg 840

13

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PATENT APPLICATION: US/09/597,796B

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122 ccaaatccga tcgggtgggg ggtcaccac cgttcatatc gggcctaccc ccttcctcgg 900
 123 cttgggtgtt gtcgacaaca acggcaacgg cgacagtc .caacgcgtgg tcggaagcgc 960
 124 tccggcggca agtctcgca tctccacccgg cgacgtgatc acccgccgtcg acggcgctcc 1020
 125 gatcaactcg gccaccgcga tggcgacgc gcttaacggg catcatcccg gtgacgtcat 1080
 126 ctcggtaac tggcaaacca agtcggcgg cacgcgtaca gggAACGTGA catggccga 1140
 127 gggacccccc gcctgatttg tcgcccgtata caccgcggg cccggccatt ggattggcgc 1200
 128 cagccgtat tgccgcgtga gcccccgagt tccgtctccc gtgcgcgtgg catgtggaa 1260
 129 gcaatgaacg aggcaaca cagcgtttag caccctccc tgcaaggcag ttacgtcga 1320
 130 ggccgtgtgg tcgacatcc ggtatccaa gacttcggca gcccgcgc cctgcccgc 1380
 131 gatccgaccc ggttaagca cccgtcttc tacgagggtgc tggccggc gtttccqac 1440
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 133 tggcttggca tcgactgcat ctgttgcgcg cgttccatcg actcaccgct gcgcgcacggc 1560
 134 gtttacgaca ttgcgcactt ctacaagggtg ctggccgaat tcggcaccgt cgacgatttc 1620
 135 gtgcgcctgg tcgacaccgc tcaccggcga ggtatccgca tcacccatcg cctgggtatg 1680
 136 aatcacaccc cggagtcgca cccctggttt caggagtcgg gcccgcaccc agacggaccc 1740
 137 tacggtgact attacgtgtg gagcgcacacc agcgcgcgtt acaccgcgc cccgatcato 1800
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 139 gcaccgattc tt 1872
 142 <210> SEQ ID NO: 4
 143 <211> LENGTH: 355
 144 <212> TYPE: PRT
 145 <213> ORGANISM: *Mycobacterium tuberculosis*
 147 <220> FEATURE:
 148 <223> OTHER INFORMATION: MTB32A (TbRa35FL) protein
 150 <400> SEQUENCE: 4
 151 Met Ser Asn Ser Arg Arg Arg Ser Leu Arg Trp Ser Trp Leu Leu Ser
 152 1 5 10 15
 153 Val Leu Ala Ala Val Gly Leu Gly Leu Ala Thr Ala Pro Ala Gln Ala
 154 20 25 30
 155 Ala Pro Pro Ala Leu Ser Gln Asp Arg Phe Ala Asp Phe Pro Ala Leu
 156 35 40 45
 157 Pro Leu Asp Pro Ser Ala Met Val Ala Gln Val Ala Pro Gln Val Val
 158 50 55 60
 159 Asn Ile Asn Thr Lys Leu Gly Tyr Asn Asn Ala Val Gly Ala Gly Thr
 160 65 70 75 80
 161 Gly Ile Val Ile Asp Pro Asn Gly Val Val Leu Thr Asn Asn His Val
 162 85 90 95
 163 Ile Ala Gly Ala Thr Asp Ile Asn Ala Phe Ser Val Gly Ser Gln
 164 100 105 110
 165 Thr Tyr Gly Val Asp Val Val Gly Tyr Asp Arg Thr Gln Asp Val Ala
 166 115 120 125
 167 Val Leu Gln Leu Arg Gly Ala Gly Gly Leu Pro Ser Ala Ala Ile Gly
 168 130 135 140
 169 Gly Gly Val Ala Val Gly Glu Pro Val Val Ala Met Gly Asn Ser Gly
 170 145 150 155 160
 171 Gly Gln Gly Gly Thr Pro Arg Ala Val Pro Gly Arg Val Val Ala Leu
 172 165 170 175
 173 Gly Gln Thr Val Gln Ala Ser Asp Ser Leu Thr Gly Ala Glu Glu Thr
 174 180 185 190

all item 9
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summary sheet

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175 Leu Asn Gly Leu Ile Gln Phe Asp Ala Ala Ile Gln Pro Gly Asp Ser
 176 195 200 205
 177 Gly Gly Pro Val Val Asn Gly Leu Gly Gln Val Val Gly Met Asn Thr
 178 210 215 220
 179 Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gln Gly Phe Ala
 180 225 230 235 240
 181 Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile Arg Ser Gly
 182 245 250 255
 183 Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly Leu
 184 260 265 270
 185 Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg Val Val
 186 275 280 285
 187 Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val Ile
 188 290 295 300
 189 Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala Asp
 190 305 310 315 320
 191 Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Asn Trp Gln
 192 325 330 335
 193 Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr Leu Ala Glu Gly
 194 340 345 350

195 Pro Pro Ala

196 355

199 <210> SEQ ID NO: 5

200 <211> LENGTH: 447

201 <212> TYPE: DNA

202 <213> ORGANISM: Mycobacterium tuberculosis

204 <220> FEATURE:

205 <223> OTHER INFORMATION: MTBRA12 C-terminus of MTB32A (Ra35FL)

207 <400> SEQUENCE: 5

208 cggtatgaac acggccgcgt ccgataactt ccagctgtcc cagggtggcc agggattcgc 60
 209 cattccgatc gggcaggcga tggcgtatcgcc gggccagatc cgatcgggtg ggggttcacc 120
 210 caccgttcat atcgggccta ccgccttcct cggcttgggt gttgtcgaca acaacggcaa 180
 211 cggcgacacga gtccaaacgcgc tggtcgggag cgctccggcg gcaagtctcg gcatctccac 240
 212 cggcgacgtg atcaccgcgg tcgacggcgc tccgatcaac tcggccaccc cgatggcgaa 300
 213 cgcgcttaac gggcatcatc ccggtgacgt catctcggtg aactggcaaa ccaagtcgaa 360
 214 cggcacgcgt acagggaaacg tgacattggc cgagggaccc cggcctgtat ttgtcggygg 420
 215 ataccacccg ccggccggcc aatttggaa 447

218 <210> SEQ ID NO: 6

219 <211> LENGTH: 132

220 <212> TYPE: PRT

221 <213> ORGANISM: Mycobacterium tuberculosis

223 <220> FEATURE:

224 <223> OTHER INFORMATION: MTBRA12 C-terminus of MTB32A (Ra35FL)

226 <400> SEQUENCE: 6

227 Thr Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln Gly Phe

228 1 5 10 15

229 Ala Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile Arg Ser

230 20 25 30

231 Gly Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly

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232 35 40 45
233 Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg Val
234 50 55 60
235 Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val
236 65 70 75 80
237 Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala
238 85 90 95
239 Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Asn Trp
240 100 105 110
241 Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr Leu Ala Glu
242 115 120 125
243 Gly Pro Pro Ala
244 130

247 <210> SEQ ID NO: 7

248 <211> LENGTH: 3058

249 <212> TYPE: DNA

250 <213> ORGANISM: *Mycobacterium tuberculosis*

252 <220> FEATURE:

253 <223> OTHER INFORMATION: MTB39 (TbH9) cDNA full-length

255 <400> SEQUENCE: 7

256 gatcgatacc gtcgagatgc tcggccgtt tgaggatgga gtgcacgtgt cttcgtat 60
257 ggcataccca gagatgttgg cggcgccgc tgacaccctg cagagcatcg gtgttaccac 120
258 tggcttagc aatgccgtc cggcgcccc gacgactggg gtggccccc ccgtgtccga 180
259 tgaggtgtcg ggcgtgactg cggcgactt cggccacat gccgcgtatgt atcagtccgt 240
260 gagcgctcg gctgtgcga ttcatgacca gttcgtggcc acccttgcga gcagcgccag 300
261 ctcgtatgcg gccactgaag tcgccaatgc ggcggccggc agctaaggca ggaacagtgc 360
262 gcacgagaaa ccacgagaaa tagggacacg taatgttggg ttccggccg ttaccaccgg 420
263 agatcaactc cgcgaggatg taccccgcc cgggttcggc ctcgctgtg gccgcggctc 480
264 agatgtggg a cagcggtcg agtgcacatgt ttccggccgc gtcggcggtt cagtcgggtgg 540
265 tctgggtct gacgtgggg tcgtggatag gttcgtccgc gggctgtatg gtggcgccgg 600
266 ctcgcccgtt tgcgtgcgtgg atgagcgtca ccggggggca ggcggagctg accggccggcc 660
267 aggtccgggt tgcgtgcgtgc gcctacgaga cggcgatgg gtcgacgggtg ccccccggg 720
268 tgcgtccga gaaacgtgtc gaaactgtatgt ttctgtatgc gaccaacctc ttggggcaaa 780
269 acaccccgcc gatcgccgtc aacgaggccc aatacggcg aatgtgggcc caagacgccc 840
270 cccgcgtt tggctacgccc gccgcgacgg cgacggcgac ggcgcgtt ctcgcgttcg 900
271 aggaggccgc ggagatgacc agcgcgggtg ggctcctcg gcaaggccgccc gcggtcgagg 960
272 aggccctccga caccggccgc gcaaccagt tgcgtacaa tgcgtccca ggcgtcccg 1020
273 agctggccca gcccacgcg ggcaccacgc cttcttccaa gtcgggtggc ctgtggaaaga 1080
274 cggctcgtcc gcatcggtcg ccgtatcgca acatgtgtc gatggccaa aaccacatgt 1140
275 cgtatgaccaa ctcggtgtc tgcgtacca acacccgtt gtcgtatgtt aagggtttt 1200
276 ctccggccgc ggcggccca ggcgtgcaccc cgcggccgc aacggggtc cggcgatga 1260
277 gtcgtgtgg cagctcgctg gttcttccgg gtcgtggccgg tgggggtggcc gccaacttgg 1320
278 gtcggccgc ctgcgtcggt tcgtgtccgg tgccgcggc ctggcccg gccaaccagg 1380
279 cagtcacccc ggcggccgc ggcgtgcgc tgaccacgt gaccaggccc gcgaaagag 1440
280 ggcggccgc gatgtgggc gggctgcggg tggggcagat gggcgccagg gccgggtgg 1500
281 ggctcagtgg tgcgtgcgt gttccgcgc gaccctatgt gatgcgcac tctccggccg 1560
282 cccgcgtacca gaggggccgc agactgtgtc tatttgcacca gtcgtaccc gtcgtgtgt 1620
283 ttccggccgc ggcgtatgaca acatgtacatg tgcgtacccaa gttacaggta ttaggtccag 1680
284 gttcaacaag gagacaggca acatggccctc acgtttatg acggatccgc acgcgtatgc 1740

09,597,796B

6

<210> 10

<211> 596

<212> PRT

<213> Artificial Sequence

<223> Description of Artificial Sequence:fusion
protein TbH9-Ra35 (MTB59F)

<400> 10

12207 Insert this

mandatory

newer identifier
whenever 12217, 1222:

or 12237 is
shown

The types of errors shown exist throughout
the Sequence Listing. Please check subsequent
sequences for similar errors.

<210> 11
<211> 2287
<212> DNA
<213> *Mycobacterium tuberculosis*
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: fusion
protein Ra12-TbH9-Ra35 (MTB72F)

(213) can only have one response:
Artificial Sequence
or Unknown or
Scientific name
(Genus/species)

<210> 25
 <211> 851
 <212> DNA
 <213> *Mycobacterium tuberculosis*

<220>
 <223> MTB39 (TbH9) cDNA

<400> 25

ctgcagggtg gcgtggatga gcgtcaccgc gggcaggcc gagctgaccg cgcggcagg 60
 ccgggttgct gcggcggcct acgagacggc gtatgggctg acggtgcccc cgccgggtat 120
 cgccgagaac cgtgctgaac tggatgattct gatagcgacc aacctcttgg ggaaaacac 180
 cccggcgatc gcggtcaacg aggccgaata cggcgagatg tgggccaag acggccggc 240
 gatgtttggc tacgcccggc cgacggcgac ggcgacggcg acgttgctgc cggtcgagg 300
 ggcgcccggag atgaccagcg cgggtgggct cctcgagcag gccgcccgg tcgaggaggc 360
 ctccgacacc gccgcggcga accagttgat gaacaatgtg ccccaaggc tgaacagtt 420
 ggcggcggcc acgcaggca ccacgccttc ttccaaagctg ggtggcctgt ggaagacgg 480
 ctgcggcat cggtcggcga tcaagcaacat ggtgtcgatg gccaacaacc acatgtcgat 540
 gaccaactcg ggtgtgtcgatg tgaccaacac cttgagctcg atgttgaagg gctttgctcc 600
 ggcggcggcc gcccaggccg tgcaaaaccgc ggcgaaaaac ggggtccggg cgatgagetc 660
 gctgggcagc tcgctgggtt cttcggtct gggcggtggg gtggccgcca acttgggtcg 720
 ggcggcctcg gtacggatag gtcaccggga tggcgaaaaa tatgc~~aa~~gt ctqqt~~cc~~q 780
 gaaacagggtt ccggcgtaag gtttacccccc gtttcttggatgcggtaac ttcgtcaacg 840
 gaaacagttt c 851

? see

item 9
 on Error
 Summary
 Sheet

IMPORTANT
 ↗

None of n or Xaa has been detected in the Sequence Listing.
 Review the Sequence Listing to insure a corresponding
 explanation is presented in the <220> to <223> fields of
 each sequence using n or Xaa.

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/597,796B

DATE: 01/15/2002
TIME: 12:32:11

Input Set : A:\-90-5.app
Output Set: N:\CRF3\01152002\I597796B.raw

L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:132 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:3
L:132 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:3
L:132 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:138 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:3
L:138 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:3
L:138 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:421 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:508 M:280 W: Numeric Identifier already exists, Organism not replaced.
L:535 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:572 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:580 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:788 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:798 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:804 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:805 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:1082 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:25
L:1082 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:25
L:1082 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25
L:1126 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:26
L:1126 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:26
L:1126 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26
L:1181 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27